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Fig-1

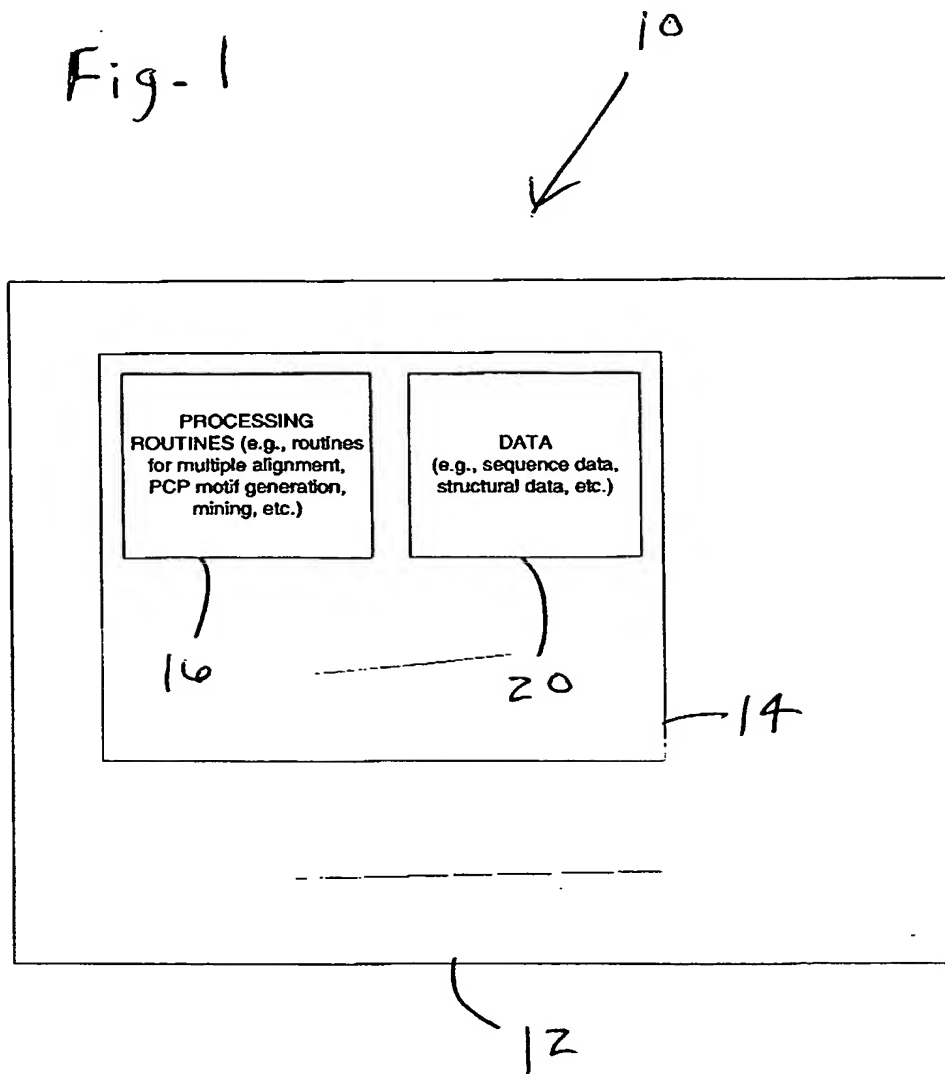
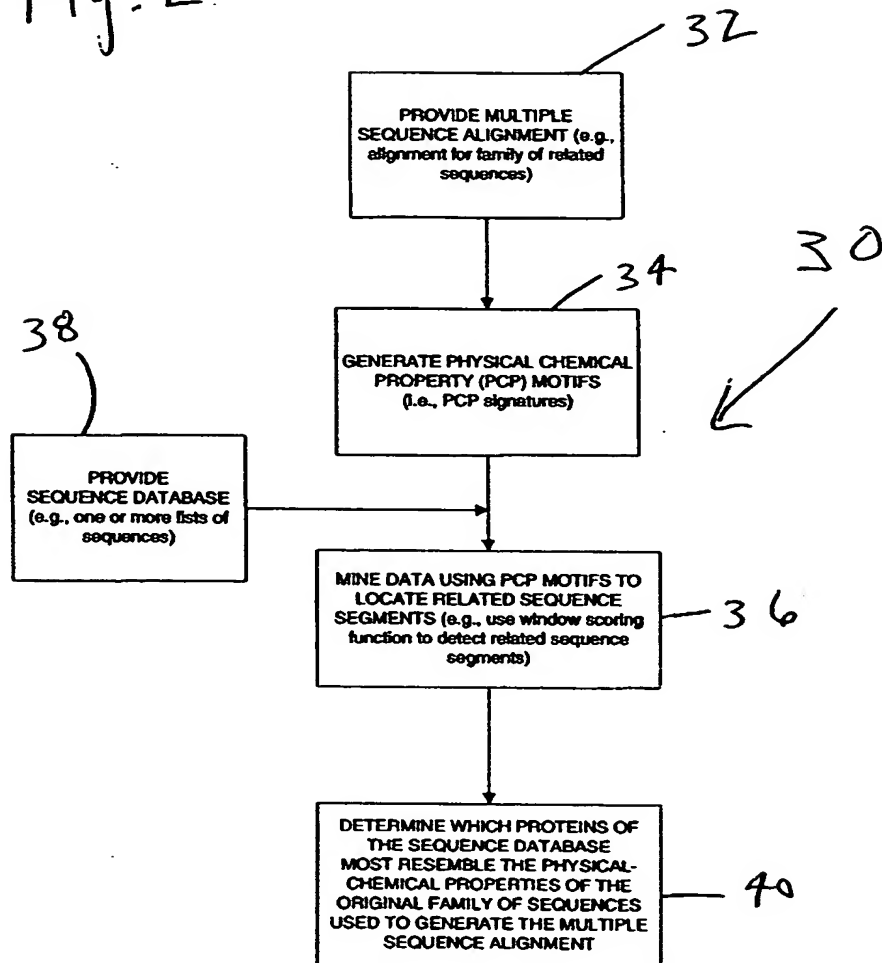


Fig. 2



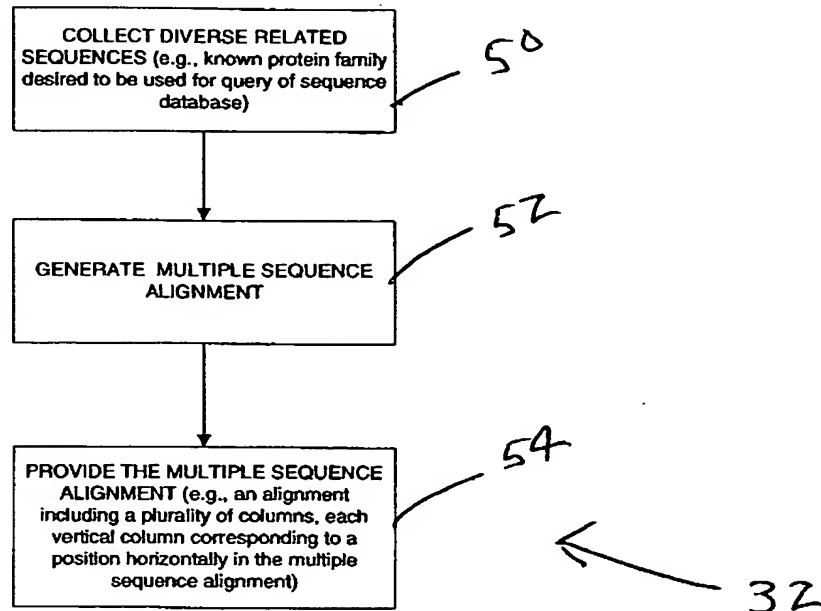


Fig. 3

Fig. 4

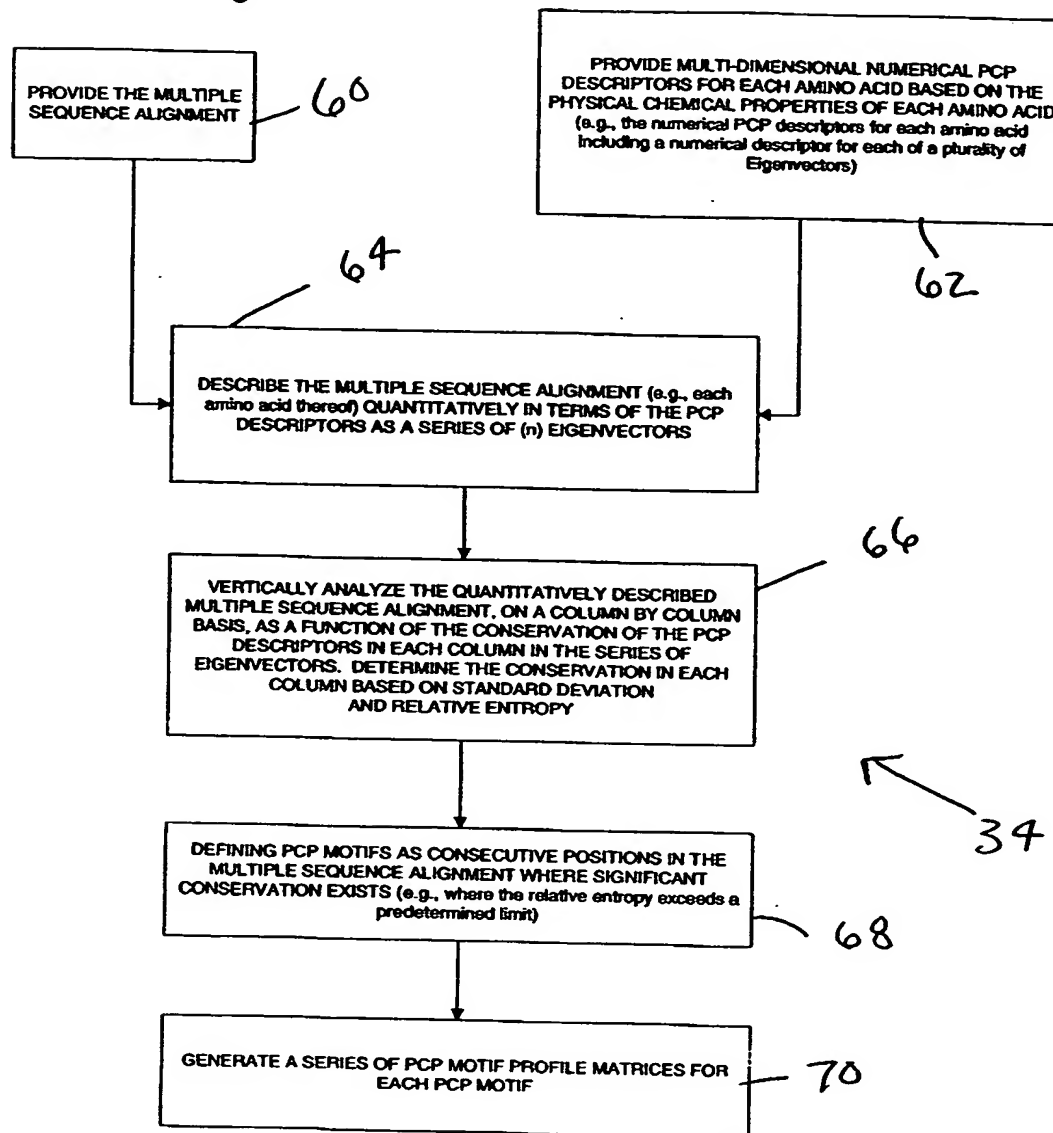


Fig. 5

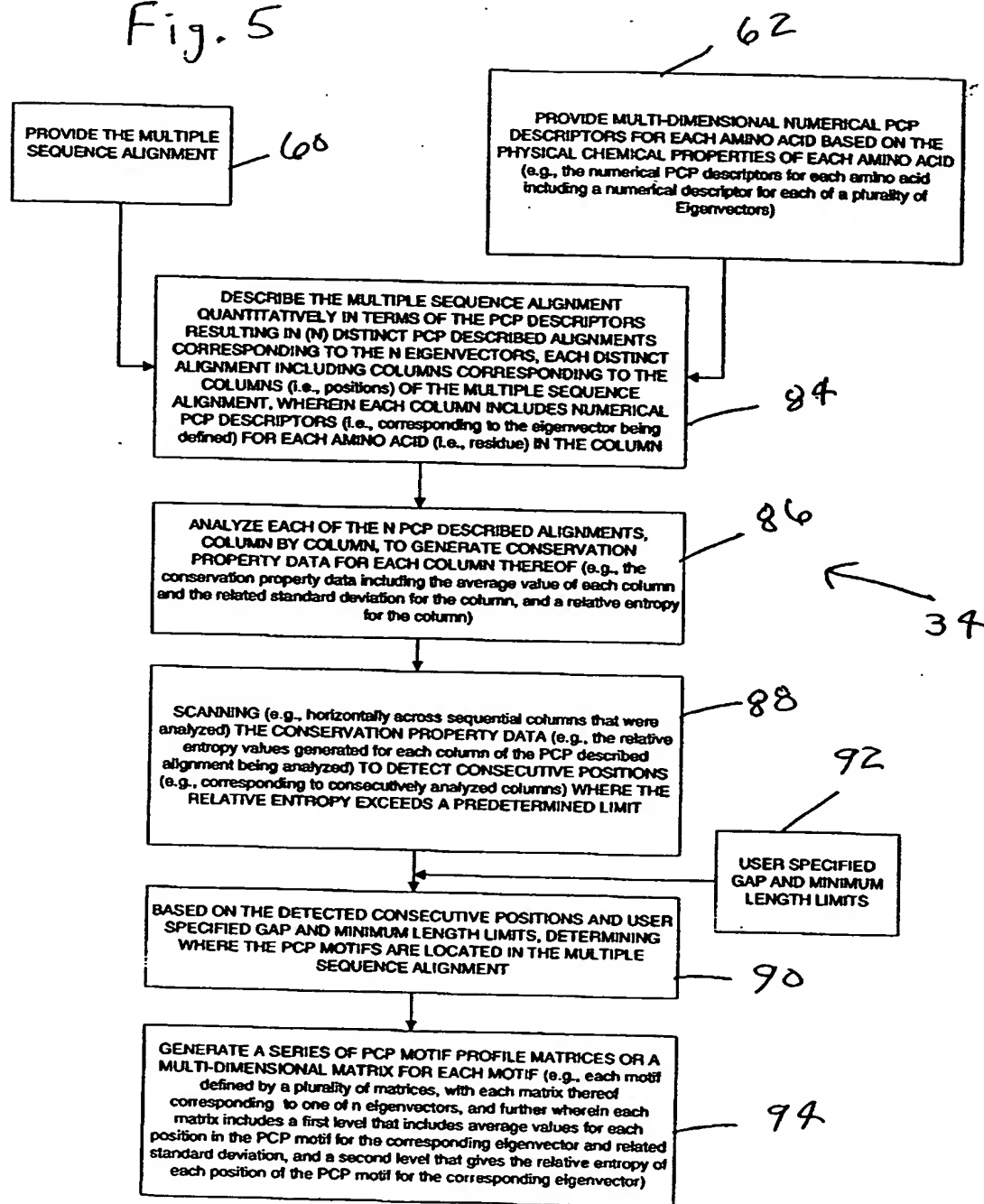


Fig. 6

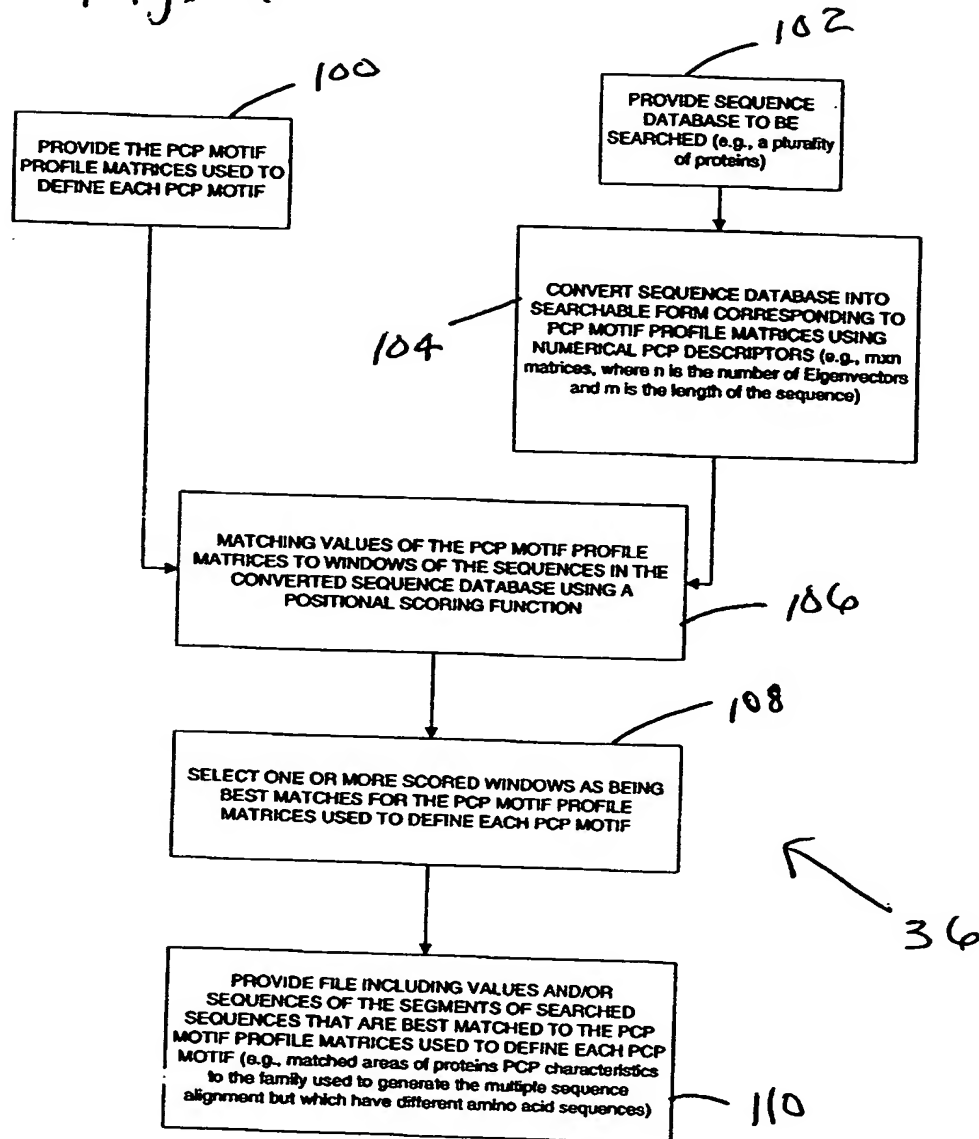


Fig. 7

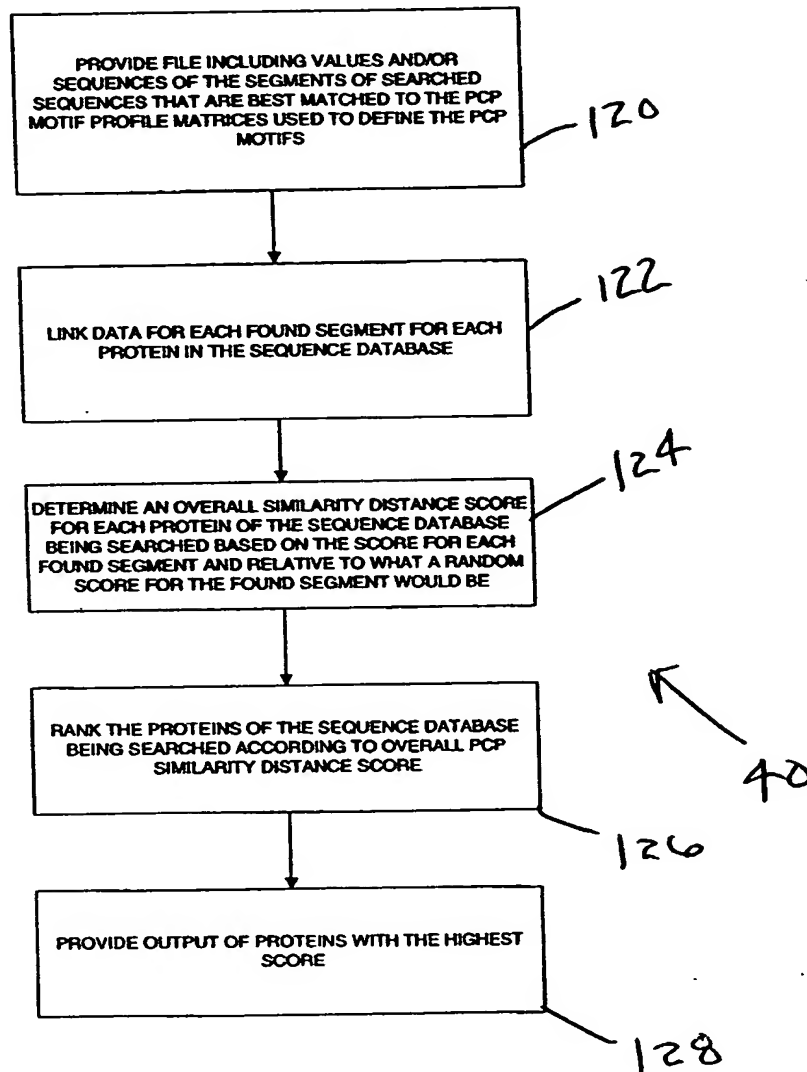
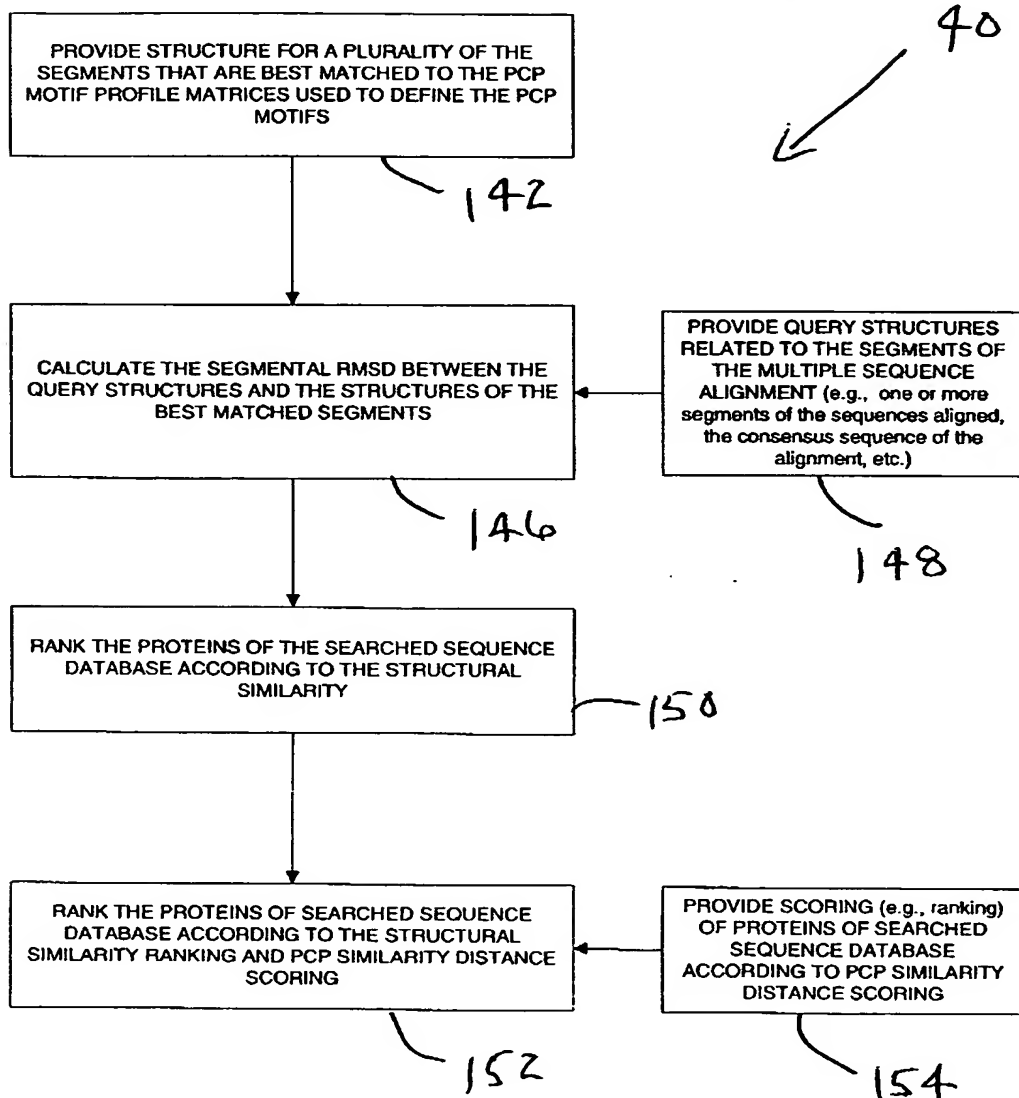




Fig. 8



| Motif No. | Query sequence (human APE)      | (S1)  | (S2)  | (S3)  | (S4)  | 42 APE score<br>ave. $\pm$ std. dev | ASTRAL40<br>ave. $\pm$ std. dev |
|-----------|---------------------------------|-------|-------|-------|-------|-------------------------------------|---------------------------------|
| 1         | 62 LKICSWNVVDGLRA 74            | 0.91* | 0.90* | 0.63* | 0.73* | 0.87 $\pm$ 0.05                     | 0.56 $\pm$ 0.05                 |
| 2         | 89 PDILCLQETK 98                | 0.96* | 0.93* | 0.84* | 0.70* | 0.92 $\pm$ 0.04                     | 0.61 $\pm$ 0.07                 |
| 3         | 125 KEGYSGVGLSRQCP 139          | 0.91* | 0.86* | 0.60  | 0.66  | 0.85 $\pm$ 0.06                     | 0.64 $\pm$ 0.05                 |
| 4         | 145 GIGDEBHDQEGRVIVAEFDSFVL 169 | 0.94* | 0.77* | 0.71  | 0.81  | 0.84 $\pm$ 0.09                     | 0.67 $\pm$ 0.07                 |
| 5         | 171 YVPNA 175                   | 0.96* | 0.96* | 0.68  | 0.86  | 0.94 $\pm$ 0.06                     | 0.68 $\pm$ 0.13                 |
| 6         | 181 RLEYRQRW 188                | 0.80* | 0.70* | 0.78  | 0.77  | 0.74 $\pm$ 0.06                     | 0.67 $\pm$ 0.05                 |
| 7         | 204 PLVLCGDLNVAH 215            | 0.96* | 0.88* | 0.82* | 0.78* | 0.90 $\pm$ 0.04                     | 0.55 $\pm$ 0.08                 |
| 8         | 231 GFTPQERQFGEL 243            | 0.96* | 0.91* | 0.78  | 0.73  | 0.87 $\pm$ 0.09                     | 0.70 $\pm$ 0.07                 |
| 9         | 247 VPLADSR 254                 | 0.96* | 0.93* | 0.70  | 0.83  | 0.91 $\pm$ 0.08                     | 0.74 $\pm$ 0.11                 |
| 10        | 264 YTFWTYM 270                 | 0.86* | 0.77* | 0.61  | 0.70  | 0.84 $\pm$ 0.08                     | 0.61 $\pm$ 0.06                 |
| 11        | 274 RSKNVGWRDYLISHSL 291        | 0.92* | 0.89* | 0.56  | 0.64  | 0.90 $\pm$ 0.04                     | 0.54 $\pm$ 0.07                 |
| 12        | 306 GSDHCP 312                  | 0.93* | 0.94* | 0.88* | 0.83* | 0.92 $\pm$ 0.03                     | 0.52 $\pm$ 0.09                 |

Fig. 9A

| PDB <sup>1</sup> | Score in bits<br>(fraction to<br>the highest<br>score) | Motifs found               | SCOP <sup>2</sup> | EC <sup>3</sup> | Description                                 |
|------------------|--|----------------------------|-------------------|-----------------|---|
| IHD7             | 1942 (1.00)  | 1,2,3,4,5,6,7,8,9,10,11,12 | d.151.1.1         | 4.2.99.18       | APE   |
| IAGO             | 1861 (0.96)  | 1,2,3,4,5,7,8,9,10,11,12   | d.151.1.1         | 3.1.11.2        | Exonuclease III                             |
| 2DNJ             | 1094 (0.56)  | 2,6,7,12                   | d.151.1.1         | 0.0.0.0         | Deoxyribonuclease I                         |
| 119Y             | 1056 (0.54)  | 1,4,5,6,7,9,12             | d.151.1.2         | 0.0.0.0         | Phosphatidylinositol phosphate Synaptojanin |
| IB3U             | 840 (0.43)   | 5,7,9,12                   | a.118.1.2         | 0.0.0.0         | Regulatory domain of protein phosphatase    |
| IMDA             | 814 (0.42)   | 6,9,11,12                  | b.69.2.1          | 1.4.99.3        | Methylamine dehydrogenase                   |
| IMPY             | 797 (0.41)   | 7,9,12                     | d.32.1.3          | 1.13.11.2       | Catechol 2,3-dioxygenase                    |
| IEKM             | 792 (0.41)   | 6,7,12                     | b.30.2.1          | 1.4.3.6         | Copper amine oxidase                        |
| IYRG             | 737 (0.38)   | 2,9,12                     | c.10.1.2          | 0.0.0.0         | Gpase RNAI                                  |
| 1QQ9             | 698 (0.36)   | 5,6,12                     | c.56.5.4          | 3.4.11.-        | Aminopeptidase                              |

<sup>1</sup>SCOP code and d.151.1 is the DNaseI superfamily code

<sup>2</sup>Enzyme commission classification number

Fig. 9B

| PDB <sup>1</sup>        | Score in bits<br>(fraction to<br>the highest<br>score) | MOLEGOS found              | SCOP <sup>2</sup> | EC <sup>3</sup> | Description                                       |
|-------------------------|--|----------------------------|-------------------|-----------------|---|
| 1HD7                    | 1942 (1.00)  | 1,2,3,4,5,6,7,8,9,10,11,12 | d.151.1.1         | 4.2.99.18       | APB (Mn/Mg/Pb)                                    |
| 1AKO                    | 1831 (0.94)  | 1,2,3,5,6,7,8,9,10,11,12   | d.151.1.1         | 3.1.11.2        | Exonuclease III                                   |
| 2DNJ                    | 1072 (0.55)  | 1,2,5,6,7,9,10,12          | d.151.1.1         | 3.1.21.1        | Deoxyribonuclease I                               |
| 119Y                    | 971 (0.50)   | 1,2,5,6,7,9,10,12          | d.151.1.2         |                 | Phosphatidylinositol phosphate Synaptotagmin      |
| 1QQ9                    | 698 (0.36)   | 5,6,9,10,12                | c.56.5.4          | 3.4.11.-        | Aminopeptidase (Zn, Ca)                           |
| 1ATL                    | 633 (0.33)   | 5,6,9,10,12                | d.92.1.9          | 3.4.24.42       | Snake venom metalloprotease (Zn, Ca)              |
| 1D09                    | 619 (0.32)   | 5,9,12                     | d.58.2.1          | 2.1.3.2         | Aspartate carboxyltransferase (Zn)                |
| 1D2N                    | 613 (0.32)   | 5,6,8,9,12                 | c.37.1.13         |                 | N-ethylmaleimide of sensitive fusion protein (Mg) |
| 1D0B                    | 579 (0.30)   | 2,5,9,12                   | c.10.2.1          |                 | InternalinB LRR domain (Ca)                       |
| 1EBM                    | 571 (0.29)   | 5,6,8,12                   | a.45.1.1          |                 | Glutathione S-transferase                         |
| PDB code of the protein |  |                            |                   |                 |   |

<sup>2</sup>SCOP code and d.151.1 is the DNaseI superfamily code

<sup>3</sup>Enzyme commission classification number

Fig- 9c

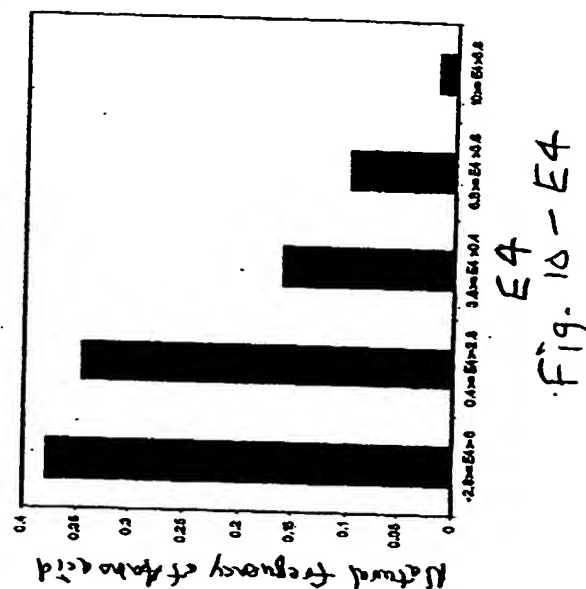
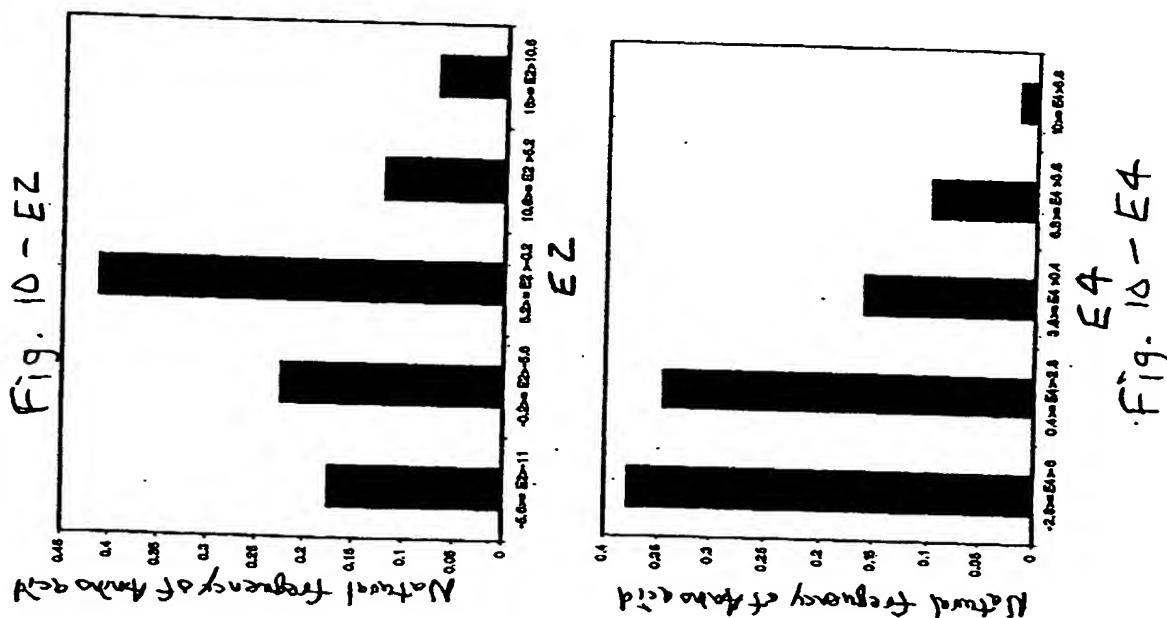
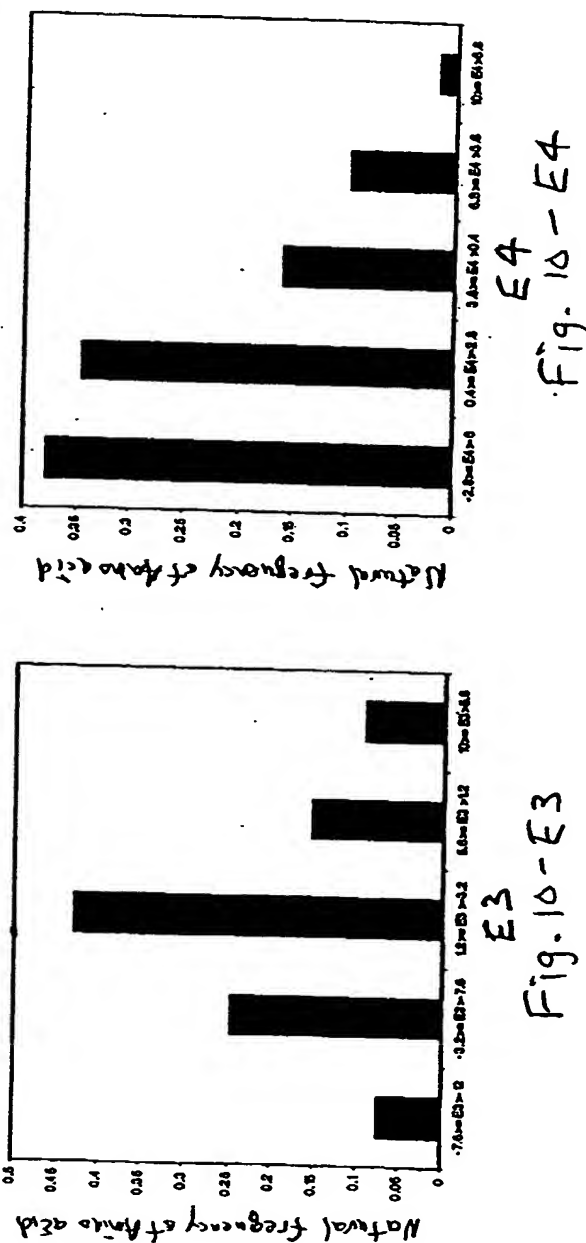
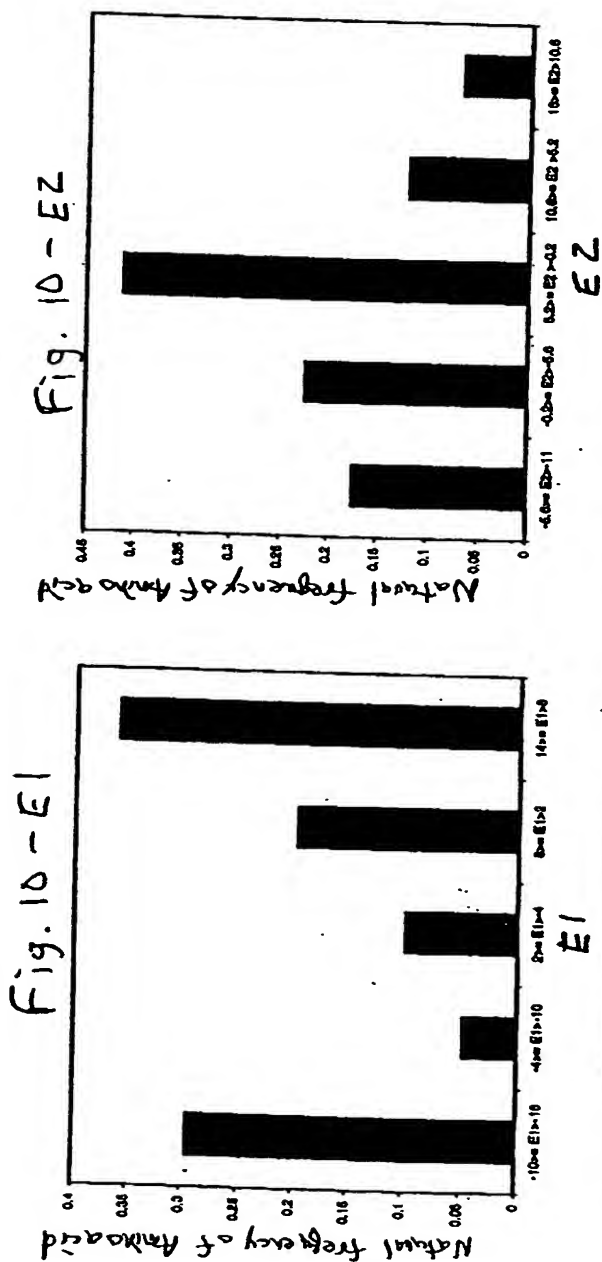
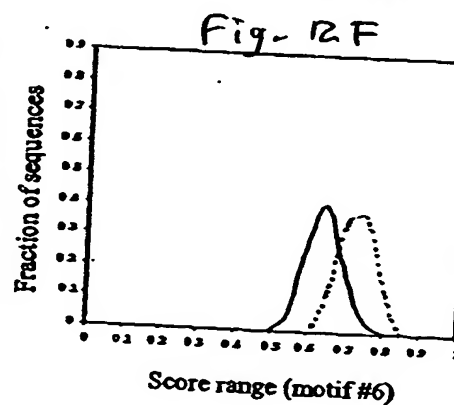
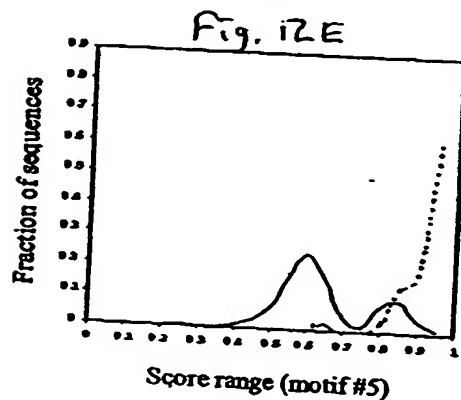
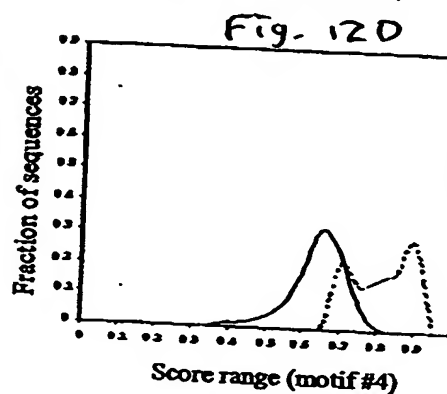
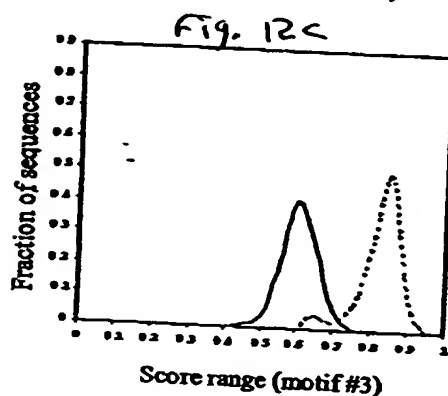
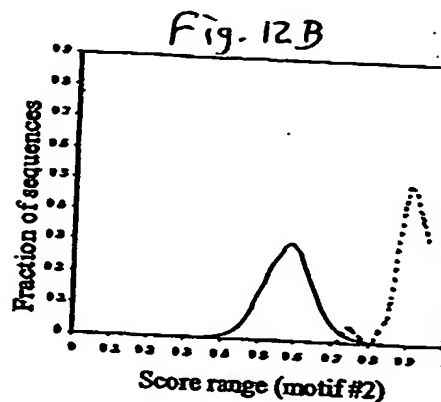
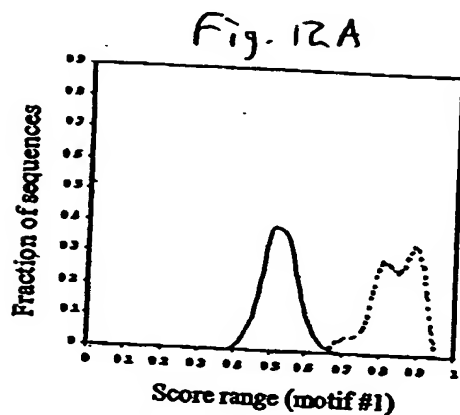


Fig. 11

|    | P | D | I | L | C | L | Q | E | T | K |
|----|---|---|---|---|---|---|---|---|---|---|
| E1 | * | + | - | - | - | - | + | + | * | * |
| E2 | * | - | * | * | * | * | - | - | * | - |
| E3 | + | * | * | * | * | * | * | - | * | * |
| E4 | * | + | * | * | + | * | + | + | * | - |
| E5 | * | + | * | * | * | * | - | + | * | - |



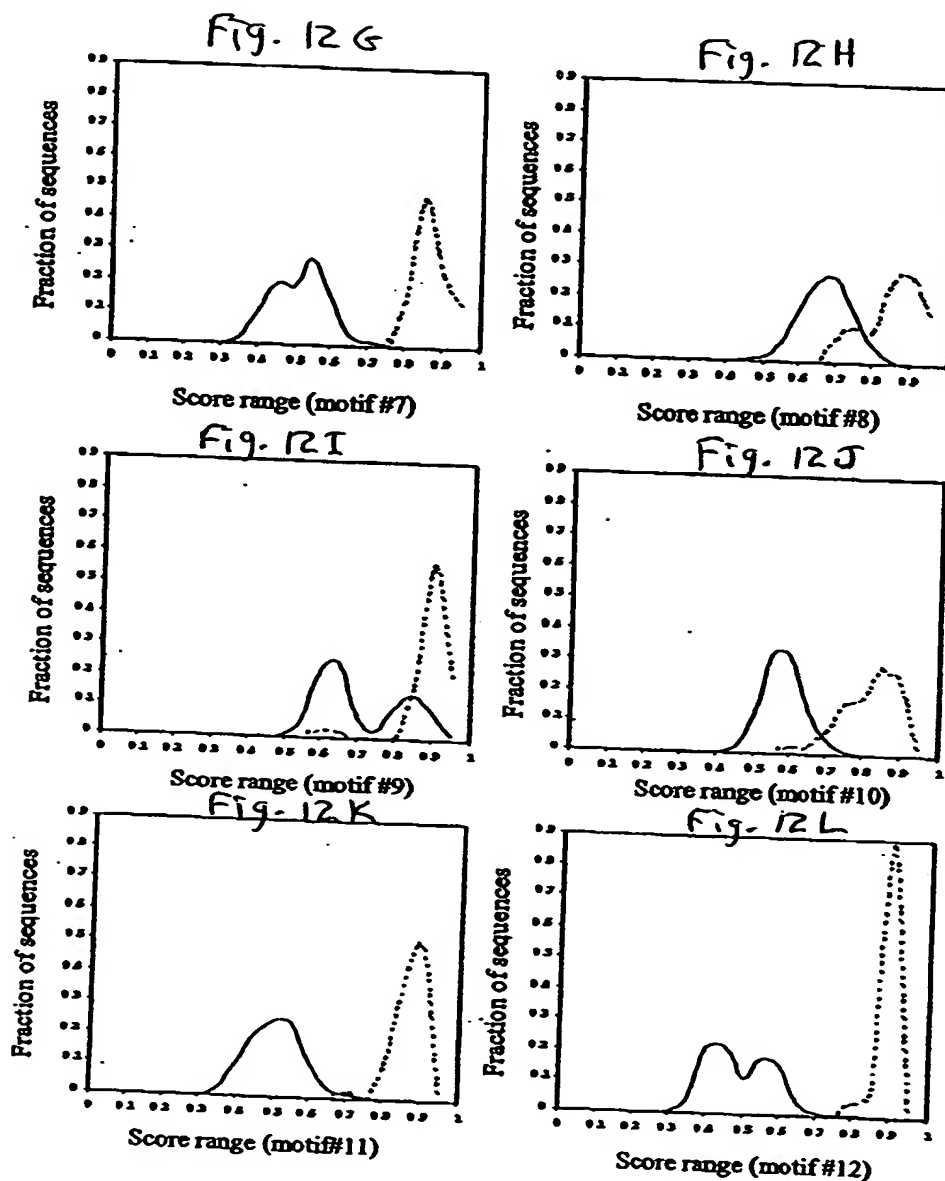




Fig. 13

1bix .....LYEDPPDQKTSFSPCKPATLKCISWVVDGLRW.....IKKKGILNWK.EA  
1ako .....HAFVSVMIRGLAR.....P..HOLEATVKEHQ  
3dni .....LXIAAFMIRTPG.....LmsnatLASTIVRIVE...R  
119yA ydphayvnhelzkrenafseHKV...VASTHNG...CS.....ATTK.LERNLP.Po

2  
1bix .....DILCLOSTK.....CSREKL.P..AKLOEL.....PGLSHQYWS.APSD  
1ako .....DVIGLOSTK.....VHDDMF.P..LEVAEL.....G..YHVFYH.G...  
3dni .....DIVLIQEVK.....DSHLVAVG..KLIDYL.....ngddpETH.YVVBpLGR  
119yA htpLadiYVVGQKIValtAADPAkrrweSCVKLLngkctsgpgIVQLRSQQL.V...

3  
1bix .....KQYSGVGLLR...QCP.....LKVSTGIGDE...KEDQE.GKVIVAEFD.....  
1ako .....QGHYCVALLAK...ETP.....IAYKROFFGO...DKKAGRIIMAKIP...sl  
3dni .....NSTKRYLFLFpknKVSU.....LDITQ.YDDGccpndSFR...KPAVVKFSshstk  
119yA .....GTALMIF...ChesolpsiknVEGTVKK.....tGLGM.KCAVAIRFD...ye

4  
1bix .....SFVLVTAYVPHACGLV...ELETRQNDKAFKIFLEG.....LA...S.RK...PLVL  
1ako lqsvTVINGYFPQGESRDEpikFFAKAQFTQKLOMLET.....EL...KIDN...FVLI  
3dni vKFAIVALHSAPS.....DAVAKDSLYDVILD.....VQqkWH.LN.DVBL  
119yA dtGLCFITSHLAAGY.....TWYDERDHYRTIASglfrfrrySI...F.NK...YVVM

5  
1bix .....GDLNVAKKEIDLEW...FPCMK...KMACFTPO.....KROCF  
1ako .....SCDHILSPDLDIGIGeenEKKWLrtGECSPLE.....ERENM  
3dni .....SCDFHAD.....CSYVTS.....QWSS.  
119yA YGDFNY.....RISLtyeavvpclagklsylfeydqlNRQM

6  
1bix .....G..ELLQAVFLADSPRELIPWTFYATTFWT...MMARSKV...GMRLDYFLSHS.LL  
1ako D..RLMSW.GLVDITFKAHPQTADGFENFDY..RSKGFDDNR...GLRIDLLASQP.LA  
3dni I..RLTSSTFQWLIP.....dsADTFAT.....ST...NCAVDRIVVAGSLQ  
119yA LtqKVVP...YFSELYI.....tFPPTTAFDigtDIYDTSdhrvPANTDRILYRGE.L.

7  
1bix .....PALC..DSKIRSKA.....L...SSDEP...LYLAL  
1ako ECCV..ETGIDYKI.....RsmekPSDEAPWATFR  
3dni SSVVpSAAFPDFQaayplamala.....ISDHYPVEVLT  
119yA .VPE..STQSV.PL.....Y...YSDHRP.YATIRAnivkvdrkkilfeel

8  
1bix .....  
1ako .....  
3dni .....  
119yA ynqrkqevrdasq

Fig. 14

